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UNITED STATES DISTRICT COURT
SOUTHERN DISTRICT OF CALIFORNIA

18 ILLUMINA, INC. and ILLUMINA
19 CAMBRIDGE LTD..

30 Plaintiffs.

21 || v.

22 || COMPLETE GENOMICS, INC

23 || Defendant

Case No. 3:12-cv-01465-BEN-BGS

JOINT CLAIM CONSTRUCTION WORKSHEET

[Patent L.R. 4-2(b)]

Hon. Roger T. Benitez

Date: July 11, 2018

Time: 9:0

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JOINT CLAIM CONSTRUCTION WORKSHEET

Claim 1	Agreed Proposed Construction	Plaintiffs' Proposed Construction	Defendant's Proposed Construction	Court's Construction
<p>A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and reading from a first primer, removing the first primer followed by hybridising and reading from a second primer at a different location in the same target double stranded polynucleotide.</p>	n/a	<p>“first and second regions” means “two distinct and separate single-stranded portions”</p>	<p>“first and second regions” means “two distinct portions of the target double-stranded polynucleotide for sequence determination. The first and second regions for sequence determination are either on the same strand, or on complementary strands, of the double-stranded polynucleotide template.”</p>	

Claim 1	Agreed Proposed Construction	Plaintiffs' Proposed Construction	Defendant's Proposed Construction	Court's Construction
<p>A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are <u>in the same target double stranded polynucleotide</u>, the method comprising hybridising and reading from a first primer, removing the first primer followed by hybridising and reading from a second primer at a different location <u>in the same target double stranded polynucleotide</u>.</p>	n/a	<p>“in the same target double stranded polynucleotide” means “in the same strand or complementary strands derived from the original polynucleotide duplex from which sequencing information is desired”</p>	<p>“in the same target double stranded polynucleotide” means “in the template polynucleotide duplex formed from complementary first and second template strands which are linked to the solid support at or near their 5' ends”</p>	
<p>A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising <u>hybridising</u> and reading from <u>a first primer</u>, removing the first primer followed by <u>hybridising</u> and reading from <u>a second primer</u> at a different location in the same target double stranded polynucleotide.</p>	<p>“hybridising ... a ... primer” means “contacting the primer and template strand under conditions which promote annealing of primer to template”</p>	n/a	n/a	

Claim 1	Agreed Proposed Construction	Plaintiffs' Proposed Construction	Defendant's Proposed Construction	Court's Construction
A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and <u>reading from a first primer</u> , removing the first primer followed by hybridising and <u>reading from a second primer</u> at a different location in the same target double stranded polynucleotide.	n/a	“reading from a [first/second] primer” means “obtaining sequence information near where the [first/second] primer has hybridized”	“reading from a [first/second] primer” means “the successive incorporation of nucleotides into a polynucleotide chain synthesized in the 5' to 3' direction from the [first/second] primer and the determination of the nature of the nucleotide after each incorporation”	
A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and reading from a first primer, <u>removing the first primer</u> followed by hybridising and reading from a second primer at a different location in the same target double stranded polynucleotide.	n/a	“removing the first primer” need not be construed, or if construed, the Court should construe this phrase as having its plain and ordinary meaning.	“removing the first primer” means “heating or chemically denaturing from the surface the first sequencing primer when the first sequencing reaction is complete.”	

Claim 1	Agreed Proposed Construction	Plaintiffs' Proposed Construction	Defendant's Proposed Construction	Court's Construction
<p>A method for pairwise sequencing of first and second regions of a double stranded polynucleotide wherein said first and second regions are in the same target double stranded polynucleotide, the method comprising hybridising and reading from a first primer, removing the first primer followed by hybridising and reading from a second primer at a <u>different location</u> in the same target double stranded polynucleotide.</p>	n/a	<p>“different location” means “a location distinct and separate from the location of hybridizing and reading from the first primer”</p>	<p>“different location” means “location of the second region that is distinct from the first region”</p>	

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3 **SIGNATURE CERTIFICATION**

4 Pursuant to Section 2(f)(4) of the Electronic Case Filing Administrative
5 Policies and Procedures Manual, I hereby certify that the content of this document
6 is acceptable to Michael J. Malecek, counsel for Defendant and Counterclaimant
7 Complete Genomics, Inc., and that I have obtained Mr. Malecek's authorization to
8 affix his electronic signature to this document.

9
10 Dated: April 16, 2013

Respectfully submitted,
11 MARSHALL, GERSTEIN & BORUN LLP

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